



FIG. 2A-1

1	M	P	I	L	S	L	C	T	I	C	S	D	F	F	D	H	S	R	D	V	A	A	I	H	C	G	H	T	F	H	mTRIP	
1	-	-	-	R	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	D	-	-	-	-	-	hTRIP		
31	L	Q	C	L	I	Q	W	F	E	T	A	P	S	R	T	C	P	Q	C	R	I	Q	V	G	K	K	R	T	I	I	N	mTRIP
31	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hTRIP		
61	K	L	F	F	D	I	A	Q	E	E	E	N	V	L	D	A	E	F	I	K	N	E	I	D	S	V	K	A	Q	I	mTRIP	
61	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	N	-	R	-	-	-	hTRIP		
91	S	Q	K	D	R	E	K	R	D	S	Q	A	I	I	D	T	I	R	D	T	I	E	E	R	N	A	T	V	E	S	mTRIP	
91	-	-	-	-	K	-	-	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	-	hTRIP		
121	I	Q	N	A	I	N	K	A	E	M	L	C	S	T	I	K	K	Q	M	K	F	I	E	Q	R	Q	D	E	T	K	mTRIP	
121	-	-	Q	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	-	-	Q	-	-	-	-	-	hTRIP		
151	Q	A	R	E	E	A	H	R	L	K	C	K	M	K	T	M	E	Q	I	E	L	L	Q	S	Q	R	S	E	V	mTRIP		
151	-	-	Q	-	-	-	G	-	-	R	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	P	-	hTRIP		
181	E	E	M	I	R	D	M	G	V	G	Q	S	A	V	E	Q	L	A	V	Y	C	V	S	L	K	K	E	Y	E	N	mTRIP	
181	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hTRIP		
211	L	K	E	A	R	K	A	T	G	E	L	A	D	R	L	K	K	D	L	V	S	S	R	S	K	L	K	T	L	N	mTRIP	
211	-	-	-	-	-	-	-	S	-	-	V	-	-	K	-	R	-	-	F	-	-	-	-	-	-	-	Q	-	V	Y	hTRIP	
241	T	E	L	D	Q	A	K	L	E	L	R	S	A	Q	K	D	L	Q	S	A	D	Q	E	I	T	S	L	R	K	K	mTRIP	
241	S	-	-	-	-	-	-	-	-	-	K	-	-	-	-	-	-	-	-	-	-	K	-	M	-	-	-	-	-	hTRIP		
271	S	D	D	P	P	G	N	L	E	P	A	S	A	T	N	E	T	V	S	R	L	V	F	E	S	P	A	P	V	E	mTRIP	
271	L	T	M	L	Q	E	T	-	N	L	P	P	V	A	S	-	-	-	D	-	-	-	L	-	-	-	-	-	-	-	hTRIP	
301	M	M	N	P	R	L	H	Q	R	P	F	G	D	E	I	D	L	N	T	T	F	D	V	N	T	P	P	T	Q	T	mTRIP	
301	V	-	-	L	K	-	-	-	-	S	-	R	-	D	-	-	-	-	A	-	-	-	-	D	-	-	-	A	R	P	hTRIP	



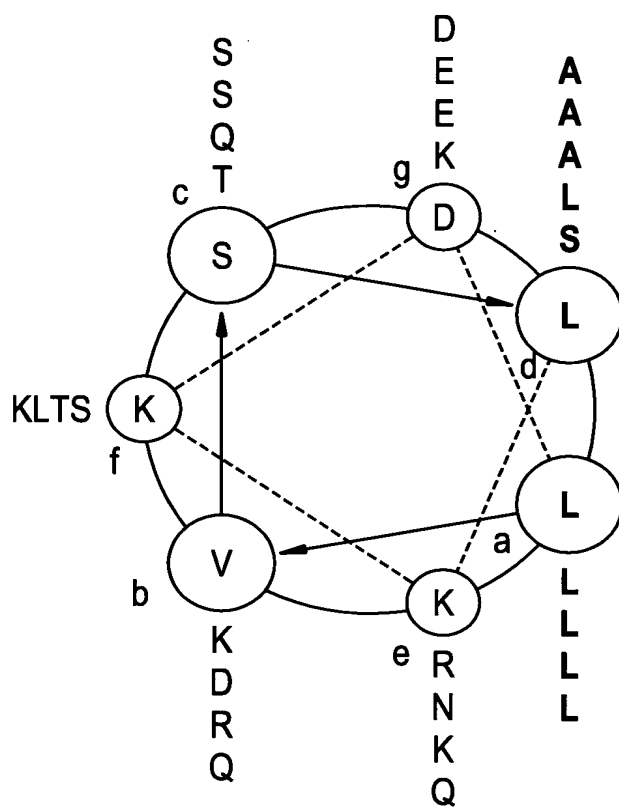


FIG. 2B

mTRIP	4	LSLCTICSDFFDHSRDVAAIHCGHTF-HLQCLIQWFETAPSRTCPQCRIQVG
hTRIP	4	RALCTICSDFFDHSRDVAAMDCGHTF-HLQCLIQSFETAPSRTCPQCRIQVG
mTRAF2	31	KYLCSACKNILLRPFQA---QCGHRY-CSFCLTSILSSGPQN-CAACVYEG
mTRAF3	48	KYKCEKCRVLVLCNPKQT---EGHRF-CESCMALLSSSPK-CTACQ-ESI
mc-IAP1	562	ERTCKVCMREVSIVFI---PCGHLVVCQECAPSLRK-----CPIGGRGTI
c-cbl	378	FQLCKICAENDKDVKIE---PCGHLM-CTSCLTSWQSEGGG-CPFCRCEIK
RING1	16	ELMCPICLDMLKNTMTTK---ECLHRF-CSDCIVTALRSGNKE-CPTCRKKLV
SS-A/Ro	13	EVTCPICLDPFVEPVSII---ECGHSF-CQECISQVGKGGSV-CAVCRQRFL
C-RZF	237	YDVCAICLDEYEDGDKLRLPCSHAY-HCKCVDPWLTTKKT-CPVCKQKV
neu	698	SAECTICYENPIDSVLY---MCGHMCYDCAIEQWRGVGGGQCLCRAVIR
consensus		...C...C...CGH...C...C...C...C...



FIG. 2C



LEUCINE ZIPPER